

## RAW SEQUENCE LISTING

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Application Serial Number: 10/522,668  
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PCT

## RAW SEQUENCE LISTING

DATE: 02/08/2005

PATENT APPLICATION: US/10/522,668

TIME: 11:47:28

Input Set : A:\Q85990 Sequence Listing.txt

Output Set: N:\CRF4\02082005\J522668.raw

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3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
4     Masayoshi TAKEDA
5     Noboru YAMAJI
7 <120> TITLE OF INVENTION: NOVEL SERINE PROTEASE
9 <130> FILE REFERENCE: Q85990
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/522,668
C--> 11 <141> CURRENT FILING DATE: 2005-01-28
11 <150> PRIOR APPLICATION NUMBER: PCT/JP03/09677
12 <151> PRIOR FILING DATE: 2003-07-30
14 <150> PRIOR APPLICATION NUMBER: JP2002-223878
15 <151> PRIOR FILING DATE: 2002-07-31
17 <160> NUMBER OF SEQ ID NOS: 26
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1596
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(1593)
31 <400> SEQUENCE: 1
32 atg gag ccc act gtg gct gac gta cac ctc gtg ccc agg aca acc aag      48
33 Met Glu Pro Thr Val Ala Asp Val His Leu Val Pro Arg Thr Thr Lys
34 1          5          10          15
36 gaa gtc ccc gct ctg gat gcc gcg tgc tgt cga gcg gcc agc att ggc      96
37 Glu Val Pro Ala Leu Asp Ala Ala Cys Cys Arg Ala Ala Ser Ile Gly
38          20          25          30
40 gtg gtg gcc acc agc ctt gtc gtc ctc acc ctg gga gtc ctt ttg gcc      144
41 Val Val Ala Thr Ser Leu Val Val Leu Thr Leu Gly Val Leu Leu Ala
42          35          40          45
44 ttc ctc tct aca cag ggc ttc cac gtg gac cac acg gcc gag ctg cgg      192
45 Phe Leu Ser Thr Gln Gly Phe His Val Asp His Thr Ala Glu Leu Arg
46          50          55          60
48 gga atc cgg tgg acc agc agt ttg cgg cgg gag acc tcg gac tat cac      240
49 Gly Ile Arg Trp Thr Ser Leu Arg Arg Thr Ser Asp Tyr His
50 65          70          75          80
52 cgc acg ctg acg ccc acc ctg gag gca ctg ttt gta agt agt ttt cag      288
53 Arg Thr Leu Thr Pro Thr Leu Glu Ala Leu Phe Val Ser Ser Phe Gln
54          85          90          95
56 aag aca gag tta gag gca agc tgc gtg ggt tgc tcg gta ctg aat tat      336
57 Lys Thr Glu Leu Glu Ala Ser Cys Val Gly Cys Ser Val Leu Asn Tyr
58          100         105         110
60 agg gat ggg aac tcc agt gtc ctc gta cat ttc cag ctg cac ttt ctg      384

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61 Arg Asp Gly Asn Ser Ser Val Leu Val His Phe Gln Leu His Phe Leu
62      115      120      125
64 ctg cga ccc ctc cag acg ctg agc ctg ggc ctg gag gag gag cta ttg      432
65 Leu Arg Pro Leu Gln Thr Leu Ser Leu Gly Leu Glu Glu Glu Leu Leu
66      130      135      140
68 cag cga ggg atc cgg gca agg ctg cgg gag cac ggc atc tcc ctg gct      480
69 Gln Arg Gly Ile Arg Ala Arg Leu Arg Glu His Gly Ile Ser Leu Ala
70 145      150      155      160
72 gcc tat ggc aca att gtg tcg gct gag ctc aca ggg aga cat aag gga      528
73 Ala Tyr Gly Thr Ile Val Ser Ala Glu Leu Thr Gly Arg His Lys Gly
74      165      170      175
76 ccc ttg gca gaa aga gac ttc aaa tca ggc cgc tgt cca ggg aac tcc      576
77 Pro Leu Ala Glu Arg Asp Phe Lys Ser Gly Arg Cys Pro Gly Asn Ser
78      180      185      190
80 ttt tcc tgc ggg aac agc cag tgt gtg acc aag gtg aac ccg gag tgt      624
81 Phe Ser Cys Gly Asn Ser Gln Cys Val Thr Lys Val Asn Pro Glu Cys
82      195      200      205
84 gac gac cag gag gac tgc tcc gat ggg tcc gac gag gcg cac tgc gag      672
85 Asp Asp Gln Glu Asp Cys Ser Asp Gly Ser Asp Glu Ala His Cys Glu
86      210      215      220
88 tgt ggc ttg cag cct gcc tgg agg atg gcc ggc agg atc gtg ggc ggc      720
89 Cys Gly Leu Gln Pro Ala Trp Arg Met Ala Gly Arg Ile Val Gly Gly
90 225      230      235      240
92 atg gaa gca tcc ccg ggg gag ttt ccg tgg caa gcc agc ctt cga gag      768
93 Met Glu Ala Ser Pro Gly Glu Phe Pro Trp Gln Ala Ser Leu Arg Glu
94      245      250      255
96 aac aag gag cac ttc tgt ggg gcc gcc atc atc aac gcc agg tgg ctg      816
97 Asn Lys Glu His Phe Cys Gly Ala Ala Ile Ile Asn Ala Arg Trp Leu
98      260      265      270
100 gtg tct gct gct cac tgc ttc aat gag ttc caa gac ccg acg aag tgg      864
101 Val Ser Ala Ala His Cys Phe Asn Glu Phe Gln Asp Pro Thr Lys Trp
102      275      280      285
104 gtg gcc tac gtg ggt gcg acc tac ctc agc ggc tcg gag gcc agc acc      912
105 Val Ala Tyr Val Gly Ala Thr Tyr Leu Ser Gly Ser Glu Ala Ser Thr
106      290      295      300
108 gtg cgg gcc cag gtg gtc cag atc gtc aag cac ccc ctg tac aac gcg      960
109 Val Arg Ala Gln Val Val Gln Ile Val Lys His Pro Leu Tyr Asn Ala
110 305      310      315      320
112 gac acg gcc gac ttt gac gtg gct gtg ctg gag ctg acc agc cct ctg      1008
113 Asp Thr Ala Asp Phe Asp Val Ala Val Leu Glu Leu Thr Ser Pro Leu
114      325      330      335
116 cct ttc ggc cgg cac atc cag ccc gtg tgc ctc ccg gct gcc aca cac      1056
117 Pro Phe Gly Arg His Ile Gln Pro Val Cys Leu Pro Ala Ala Thr His
118      340      345      350
120 atc ttc cca ccc agc aag aag tgc ctg atc tca ggc tgg ggc tac ctc      1104
121 Ile Phe Pro Pro Ser Lys Lys Cys Leu Ile Ser Gly Trp Gly Tyr Leu
122      355      360      365
124 aag gag gac ttc ctg gtc aag cca gag gtg ctg cag aaa gcc act gtg      1152
125 Lys Glu Asp Phe Leu Val Lys Pro Glu Val Leu Gln Lys Ala Thr Val

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126      370      375      380
128 gag ctg ctg gac cag gca ctg tgt gcc agc ttg tac ggc cat tca ctc      1200
129 Glu Leu Leu Asp Gln Ala Leu Cys Ala Ser Leu Tyr Gly His Ser Leu
130 385      390      395      400
132 act gac agg atg gtg tgc gct ggc tac ctg gac ggg aag gtg gac tcc      1248
133 Thr Asp Arg Met Val Cys Ala Gly Tyr Leu Asp Gly Lys Val Asp Ser
134      405      410      415
136 tgc cag ggt gac tca gga gga ccc ctg gtc tgc gag gag ccc tct ggc      1296
137 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Pro Ser Gly
138      420      425      430
140 cgg ttc ttt ctg gct ggc atc gtg agc tgg gga atc ggg tgt gcg gaa      1344
141 Arg Phe Phe Leu Ala Gly Ile Val Ser Trp Gly Ile Gly Cys Ala Glu
142      435      440      445
144 gcc cgg cgt cca ggg gtc tat gcc cga gtc acc agg cta cgt gac tgg      1392
145 Ala Arg Arg Pro Gly Val Tyr Ala Arg Val Thr Arg Leu Arg Asp Trp
146      450      455      460
148 atc ctg gag gcc acc acc aaa gcc agc atg cct ctg gcc ccc acc atg      1440
149 Ile Leu Glu Ala Thr Thr Lys Ala Ser Met Pro Leu Ala Pro Thr Met
150 465      470      475      480
152 gct cct gcc cct gcc gcc ccc agc aca gcc tgg ccc acc agt cct gag      1488
153 Ala Pro Ala Pro Ala Ala Pro Ser Thr Ala Trp Pro Thr Ser Pro Glu
154      485      490      495
156 agc cct gtg gtc agc acc ccc acc aaa tcg atg cag gcc ctc agt acc      1536
157 Ser Pro Val Val Ser Thr Pro Thr Lys Ser Met Gln Ala Leu Ser Thr
158      500      505      510
160 gtg cct ctt gac tgg gtc acc gtt cct aag cta caa ggt att ttc ggg      1584
161 Val Pro Leu Asp Trp Val Thr Val Pro Lys Leu Gln Gly Ile Phe Gly
162      515      520      525
164 gca gaa agg tag      1596
165 Ala Glu Arg
166      530
169 <210> SEQ ID NO: 2'
170 <211> LENGTH: 531
171 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 2
176 Met Glu Pro Thr Val Ala Asp Val His Leu Val Pro Arg Thr Thr Lys
177 1      5      10      15
180 Glu Val Pro Ala Leu Asp Ala Ala Cys Cys Arg Ala Ala Ser Ile Gly
181      20      25      30
184 Val Val Ala Thr Ser Leu Val Val Leu Thr Leu Gly Val Leu Leu Ala
185      35      40      45
188 Phe Leu Ser Thr Gln Gly Phe His Val Asp His Thr Ala Glu Leu Arg
189      50      55      60
192 Gly Ile Arg Trp Thr Ser Ser Leu Arg Arg Glu Thr Ser Asp Tyr His
193 65      70      75      80
196 Arg Thr Leu Thr Pro Thr Leu Glu Ala Leu Phe Val Ser Ser Phe Gln
197      85      90      95
200 Lys Thr Glu Leu Glu Ala Ser Cys Val Gly Cys Ser Val Leu Asn Tyr

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201		100		105		110
204	Arg	Asp	Gly	Asn	Ser	Ser
205		115		120		125
208	Leu	Arg	Pro	Leu	Gln	Thr
209		130		135		140
212	Gln	Arg	Gly	Ile	Arg	Ala
213	145			150		155
216	Ala	Tyr	Gly	Thr	Ile	Val
217		165		170		175
220	Pro	Leu	Ala	Glu	Arg	Asp
221		180		185		190
224	Phe	Ser	Cys	Gly	Asn	Ser
225		195		200		205
228	Asp	Asp	Gln	Glu	Asp	Cys
229		210		215		220
232	Cys	Gly	Leu	Gln	Pro	Ala
233	225			230		235
236	Met	Glu	Ala	Ser	Pro	Gly
237		245		250		255
240	Asn	Lys	Glu	His	Phe	Cys
241		260		265		270
244	Val	Ser	Ala	His	Cys	Phe
245		275		280		285
248	Val	Ala	Tyr	Val	Gly	Ala
249		290		295		300
252	Val	Arg	Ala	Gln	Val	Val
253	305			310		315
256	Asp	Thr	Ala	Asp	Phe	Asp
257		325		330		335
260	Pro	Phe	Gly	Arg	His	Ile
261		340		345		350
264	Ile	Phe	Pro	Pro	Ser	Lys
265		355		360		365
268	Lys	Glu	Asp	Phe	Leu	Val
269		370		375		380
272	Glu	Leu	Leu	Asp	Gln	Ala
273	385			390		395
276	Thr	Asp	Arg	Met	Val	Cys
277		405		410		415
280	Cys	Gln	Gly	Asp	Ser	Gly
281		420		425		430
284	Arg	Phe	Phe	Leu	Ala	Gly
285		435		440		445
288	Ala	Arg	Arg	Pro	Gly	Val
289		450		455		460
292	Ile	Leu	Glu	Ala	Thr	Thr
293	465			470		475
296	Ala	Pro	Ala	Pro	Ala	Ala
297		485		490		495

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300 Ser Pro Val Val Ser Thr Pro Thr Lys Ser Met Gln Ala Leu Ser Thr
301          500          505          510
304 Val Pro Leu Asp Trp Val Thr Val Pro Lys Leu Gln Gly Ile Phe Gly
305          515          520          525
308 Ala Glu Arg
309          530
312 <210> SEQ ID NO: 3
313 <211> LENGTH: 27
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence: an artificially
319     synthesized primer sequence
321 <400> SEQUENCE: 3
322 ccatacctaata acgactcact atagggc                                27
325 <210> SEQ ID NO: 4
326 <211> LENGTH: 23
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Description of Artificial Sequence: an artificially
332     synthesized primer sequence
334 <400> SEQUENCE: 4
335 actcactata gggctcgagc ggc                                23
338 <210> SEQ ID NO: 5
339 <211> LENGTH: 29
340 <212> TYPE: DNA
341 <213> ORGANISM: Homo sapiens
343 <400> SEQUENCE: 5
344 aggatccagt cacgtagcct ggtgactcg                                29
347 <210> SEQ ID NO: 6
348 <211> LENGTH: 31
349 <212> TYPE: DNA
350 <213> ORGANISM: Homo sapiens
352 <400> SEQUENCE: 6
353 gtagccccag cctgagatca ggcacttctt g                                31
356 <210> SEQ ID NO: 7
357 <211> LENGTH: 29
358 <212> TYPE: DNA
359 <213> ORGANISM: Homo sapiens
361 <400> SEQUENCE: 7
362 cggtgatgat ggcggcccca cagaagtgc                                29
365 <210> SEQ ID NO: 8
366 <211> LENGTH: 29
367 <212> TYPE: DNA
368 <213> ORGANISM: Homo sapiens
370 <400> SEQUENCE: 8
371 ctggaaggct ggcttgccac ggaaactcc                                29
374 <210> SEQ ID NO: 9

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**VERIFICATION SUMMARY**

DATE: 02/08/2005

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Input Set : A:\Q85990 Sequence Listing.txt

Output Set: N:\CRF4\02082005\J522668.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date